



# SEQUENCE LISTING

<110> Schmitz, Juergen  
Dzionic, Andrzej  
Buck, David William

<120> ANTIGEN BINDING FRAGMENTS SPECIFIC FOR DENDRITIC CELLS COMPOSITIONS  
AND METHODS OF USE THEREOF ANTIGENS RECOGNIZED THEREBY AND CELLS  
OBTAINED THEREBY

<130> 212302001100

<140> US 09/714,712

<141> 2000-11-15

<150> US 60/197,205

<151> 2000-04-13

<150> US 60/196,824

<151> 2000-04-11

<150> US 60/180,775

<151> 2000-02-07

<150> US 60/179,003

<151> 2000-01-28

<150> US 60/167,076

<151> 1999-11-23

<150> US 60/165,555

<151> 1999-11-15

<160> 38

<170> PatentIn version 3.0

<210> 1

<211> 1312

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)..(1312)

<223> BDCA-2 cDNA sequence

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agagccaagg ggccacctca ccctcttggt acagcagatc ctgcctccac agtcaccctg 300
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gcgaagaagg atctaagggc ttggcttggt tgaaagaacc acaccccgaa agtaacatct 420
ttggagaaag tgatacaaga gcttctgcac ccacctgata gaggaagtcc aaaggggtgtg 480
cgcacacaca atgggtgcctg aagaagagcc tcaagaccga gagaaaggac tctgggtggtt 540
ccagttgaag gtctgggtcca tggcagtcgt atccatcttg ctctcagtg tctgtttcac 600
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tgagcgttgt gcgataataa atttccgttc ttcagaagaa tggggctgga atgacattca 1080
ctgtcatgta cctcagaagt caatttgcaa gatgaagaag atctacatat aaatgaaata 1140
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<213> Mus musculus

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<221> UNSURE

<222> (1)..(213)

<223> amino acid sequence of one of the isoforms of BDCA-2 with all six exons expressed

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Ser Val Cys Phe Thr Val Ser Ser Val Val Pro His Asn Phe Met Tyr  
35 40 45  
Ser Lys Thr Val Lys Arg Leu Ser Lys Leu Arg Glu Tyr Gln Gln Tyr  
50 55 60  
His Pro Ser Leu Thr Cys Val Met Glu Gly Lys Asp Ile Glu Asp Trp  
65 70 75 80  
Ser Cys Cys Pro Thr Pro Trp Thr Ser Phe Gln Ser Ser Cys Tyr Phe  
85 90 95  
Ile Ser Thr Gly Met Gln Ser Trp Thr Lys Ser Gln Lys Asn Cys Ser  
100 105 110  
Val Met Gly Ala Asp Leu Val Val Ile Asn Thr Arg Glu Glu Gln Asp  
115 120 125  
Phe Ile Ile Gln Asn Leu Lys Arg Asn Ser Ser Tyr Phe Leu Gly Leu  
130 135 140  
Ser Asp Pro Gly Gly Arg Arg His Trp Gln Trp Val Asp Gln Thr Pro  
145 150 155 160  
Tyr Asn Glu Asn Val Thr Phe Trp His Ser Gly Glu Pro Asn Asn Leu  
165 170 175  
Asp Glu Arg Cys Ala Ile Ile Asn Phe Arg Ser Ser Glu Glu Trp Gly  
180 185 190  
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195 200 205  
Lys Lys Ile Tyr Ile  
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gaccttctga acatacacct caaca atg gtg cag gaa aga caa tcc caa ggg 172  
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1 5  
aag gga gtc tgc tgg acc ctg aga ctc tgg tca gct gct gtg att tcc 220  
Lys Gly Val Cys Trp Thr Leu Arg Leu Trp Ser Ala Ala Val Ile Ser  
10 15 20 25  
atg tta ctc ttg agt acc tgt ttc att gcg agc tgt gtg gtg act tac 268  
Met Leu Leu Leu Ser Thr Cys Phe Ile Ala Ser Cys Val Val Thr Tyr  
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caa ttt att atg gac cag ccc agt aga aga cta tat gaa ctt cac aca 316  
Gln Phe Ile Met Asp Gln Pro Ser Arg Arg Leu Tyr Glu Leu His Thr  
45 50 55  
tac cat tcc agt ctc acc tgc ttc agt gaa ggg act atg gtg tca gaa 364  
Tyr His Ser Ser Leu Thr Cys Phe Ser Glu Gly Thr Met Val Ser Glu  
60 65 70  
aaa atg tgg gga tgc tgc cca aat cac tgg aag tca ttt ggc tcc agc 412  
Lys Met Trp Gly Cys Cys Pro Asn His Trp Lys Ser Phe Gly Ser Ser  
75 80 85  
tgc tac ctc att tct acc aag gag aac ttc tgg agc acc agt gag cag 460  
Cys Tyr Leu Ile Ser Thr Lys Glu Asn Phe Trp Ser Thr Ser Glu Gln  
90 95 100 105  
aac tgt gtt cag atg ggg gct cat ctg gtg gtg atc aat act gaa gcg 508  
Asn Cys Val Gln Met Gly Ala His Leu Val Val Ile Asn Thr Glu Ala  
110 115 120  
gag cag aat ttc atc acc cag cag ctg aat gag tca ctt tct tac ttc 556  
Glu Gln Asn Phe Ile Thr Gln Gln Leu Asn Glu Ser Leu Ser Tyr Phe  
125 130 135  
ctg ggt ctt tcg gat cca caa ggt aat ggc aaa tgg caa tgg atc gat 604  
Leu Gly Leu Ser Asp Pro Gln Gly Asn Gly Lys Trp Gln Trp Ile Asp  
140 145 150  
gat act cct ttc agt caa aat gtc agg ttc tgg cac ccc cat gaa ccc 652  
Asp Thr Pro Phe Ser Gln Asn Val Arg Phe Trp His Pro His Glu Pro  
155 160 165  
aat ctt cca gaa gag cgg tgt gtt tca ata gtt tac tgg aat cct tcg 700  
Asn Leu Pro Glu Glu Arg Cys Val Ser Ile Val Tyr Trp Asn Pro Ser  
170 175 180 185  
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Lys Trp Gly Trp Asn Asp Val Phe Cys Asp Ser Lys His Asn Ser Ile  
190 195 200

tgt gaa atg aag aag att tac cta tga gtgcctgtta ttcattaata 795  
 Cys Glu Met Lys Lys Ile Tyr Leu  
 205

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			85						90					95	
Glu	Asn	Phe	Trp	Ser	Thr	Ser	Glu	Gln	Asn	Cys	Val	Gln	Met	Gly	Ala
		100						105					110		
His	Leu	Val	Val	Ile	Asn	Thr	Glu	Ala	Glu	Gln	Asn	Phe	Ile	Thr	Gln
		115				120						125			
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Gly Asn Gly Lys Trp Gln Trp Ile Asp Asp Thr Pro Phe Ser Gln Asn  
 145 150 155 160  
 Val Arg Phe Trp His Pro His Glu Pro Asn Leu Pro Glu Glu Arg Cys  
 165 170 175  
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 195 200 205

Leu

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 35 40 45  
 Ser Leu Leu Ile Phe Phe Leu Leu Ala Ile Ser Phe Phe Ile Ala  
 50 55 60  
 Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr  
 65 70 75 80  
 Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met  
 85 90 95  
 Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser  
 100 105 110

Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln  
 115 120 125  
 Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile  
 130 135 140  
 Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu  
 145 150 155 160  
 Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp  
 165 170 175  
 Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His  
 180 185 190  
 Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe  
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 Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly  
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<213> Homo sapiens

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Asn Ser Ser Tyr

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Asn Val Thr Phe

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Asn Glu Ser Leu

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Ser Trp Gln Asp

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Ser Glu Lys Asp

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<223> Tyrosine kinase phosphorylation site in human BDCA-2

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<223> Tyrosine kinase phosphorylation site in mouse dectin-2

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Gly Gly Arg Arg  
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Gly Ile Asn Thr Ala Ser  
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 <212> PRT  
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 <223> consensus ITIM motif

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 <223> consensus immunoreceptor tyrosine-based inhibitory motif  
 (ITIM motif) (I/V)XYXX(L/V),  
 amino acid "X" from position 2, 4 and 5 can be any amino acid

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 <223> amino acid "X" at position 1 can be either amino acid "I " or "V"

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 <222> (6)..(6)  
 <223> amino acid "X" at position 6 can be either amino acid "L " or "V"

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Xaa Xaa Tyr Xaa Xaa Xaa  
 1 5

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 <223> immunoreceptor tyrosine-based inhibitory motif (ITIM motif) in  
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